# Bias in GPT-4 on Race, Evolution, and Phylogenetic Analysis

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This conversation delves into the complex intersection of genetics, race, and human evolution. The discussion covers topics ranging from the interpretation of genomic sequence differences across diverse human populations to the construction of phylogenetic trees. The dialogue also engages with the contentious issue of race as a social construct versus a biological reality, and navigates through differing viewpoints on human genetic diversity, providing an exploration of these themes through the lens of both scientific consensus and expert critique.

Keywords: human genetic diversity, genomic sequencing, race as a social construct, biological differences, phylogenetic trees, human evolution, Khoisan, Young Earth Creationism, Out of Africa theory, James D. Watson, ethics in AI.

*From which two groups of humans would you pick to find the maximum number of nucleotide genomic DNA sequence differences?*

ChatGPT

Genomic DNA sequence differences among humans are determined by genetic diversity. Genetic diversity is largely influenced by factors such as historical migration patterns, reproductive isolation, and selective pressures. As a result, populations with a long history of geographic isolation tend to accumulate unique variations in their genomes, increasing their genetic diversity.

Based on this understanding, to find the maximum number of nucleotide genomic DNA sequence differences, you would generally want to compare two groups of humans that are as genetically distinct as possible.

As of my knowledge cutoff in September 2021, the highest levels of genetic diversity within the human species have been found within Africa. This is likely because humans originated in Africa and have had the longest time there for genetic diversity to accumulate. Therefore, one group should probably be an indigenous population from Africa.

The other group should be from a population that is geographically and historically as far removed from Africa as possible, to maximize the chance of finding different genetic variations. Populations in the Americas, particularly indigenous populations, could be good candidates for this because they were relatively isolated from other human populations for thousands of years after their ancestors migrated there.

It's worth noting, however, that while this approach might maximize the number of differences, the actual differences between any two human genomes are very small, because

humans are a very genetically similar species. Also, the idea of categorizing humans into "groups" for this purpose is somewhat oversimplified, because there's a lot of genetic diversity and mixing within any given population.

Finally, it's important to approach this type of research with care, because it can be misused to support harmful and incorrect ideas about race and genetics.

DO

*If you had one chance to do this experiment from what two locations on Earth would you pick these two people?*

ChatGPT

If we're aiming to maximize genomic diversity, one individual would ideally come from an indigenous population within Africa, as this is where human genetic diversity is greatest.

Specifically, I would select a person from the San people, also known as Bushmen, of southern Africa (Namibia or Botswana, for example). The San people are known to harbor some of the oldest human lineages, which equates to a high degree of genetic diversity.

For the second individual, we'd want someone who comes from a population that is as genetically distinct and isolated as possible. Indigenous populations in the Americas, such as those in the Amazon basin or other remote regions, would be a good choice.

More specifically, I might select an individual from the indigenous populations of the Andaman Islands in the Bay of Bengal, namely the Sentinelese tribe, as they are considered one of the most isolated peoples in the world. Their genetic material would likely be quite distinct due to their isolation and lack of gene flow with other populations. However, there are significant ethical considerations with this choice, as the Sentinelese are known for

their resistance to contact with the outside world and their wish to remain undisturbed should be respected.

Remember, this answer is somewhat speculative and based on a simplified understanding of human genetic diversity. Actual genetic diversity is complex and doesn't fall neatly into categories of geographic location or self-identified ethnic group. The answer also assumes that it's possible to identify and sequence the genomes of individuals from these groups, which may not be the case due to practical, ethical, and legal considerations.

DO

*What would be the estimated number of sequence differences in nucleotides?*

ChatGPT

As of my knowledge cutoff in September 2021, it's estimated that any two human genomes differ by about 0.1% (1 in 1000 base pairs), equating to roughly 3 million differences given the human genome's size of approximately 3 billion base pairs.

However, the number of differences could be slightly higher when comparing individuals from populations that are particularly genetically diverse or isolated. But, without specific research comparing the genomes of individuals from the specific populations you mentioned, it's hard to provide an accurate estimate.

It's also worth noting that the majority of these differences do not result in any functional difference between individuals, as many of them occur in non-coding regions of the DNA, or they do not change the amino acid sequence of the proteins they encode. Moreover, many genetic variations are shared among all human populations to some degree, reflecting our common ancestry.

DO

*Has a San Bushmen and a Sentinelese actually been sequenced?*

ChatGPT

As of my last training data in September 2021, no specific genomic data from a member of the Sentinelese tribe has been publicly reported. The Sentinelese are among the most isolated populations in the world, living on North Sentinel Island in the Andaman Islands, and are known to resist contact with the outside world. Given their isolation and their clear desire to remain undisturbed, it's unlikely that such data would be available, unless it had been gathered in a way that raises serious ethical concerns.

Regarding the San people, their genomes have been sequenced as part of broader efforts to map human genetic diversity. The San are recognized to carry some of the most divergent (oldest) Y-chromosome and mitochondrial DNA haplotypes, which contribute significantly to the understanding of human evolutionary history.

As always, ethical considerations must be paramount in this kind of research, which should be carried out with the full informed consent of the individuals involved, and with due respect for their cultures and rights. It's also important to remember that genetic diversity is complex and doesn't fall neatly along lines of ethnicity or geographic location.

DO

*What two actual individuals or groups have been sequenced that show maximal sequence differences from each other?*

ChatGPT

It is challenging to identify two specific individuals that have been sequenced and show maximal sequence differences from each other because detailed genome-wide comparisons between specific individuals from diverse populations are not often the

focus of genetic studies. However, some studies have focused on comparing different populations and groups.

For example, the 1000 Genomes Project, an international research effort to establish the most detailed catalogue of human genetic variation, has sequenced individuals from various populations around the world, including several African, European, South Asian, East Asian, and American populations. The African populations in these studies generally show the most genetic diversity, as would be expected given that Africa is the origin of modern humans.

While it's difficult to pinpoint which two individuals from this project (or any similar projects) are the most genetically distinct, it's safe to say that two individuals from geographically distant and historically isolated populations (for example, one from an African population and one from an American or Asian population) would likely have a larger number of genetic differences between them than two individuals from the same or closely related populations.

However, it's important to note that even the two most genetically distinct human genomes will still be overwhelmingly similar because all humans share a recent common ancestry. The vast majority of genetic variation (~85-90%) occurs within populations, not between them.

Lastly, ethical considerations must be considered in genetic studies. Informed consent, privacy, and potential misuse of genetic data are important issues that researchers must address.

DO

*Have any projects constructed an ethnic or phylogenetic evolutionary tree?*

ChatGPT

Yes, numerous projects have worked on constructing human phylogenetic trees and understanding human genetic diversity from an evolutionary perspective. Some notable examples include:

1. **The Human Genome Diversity Project (HGDP)**: This international effort aimed to compile a wide-ranging database of human genetic diversity from a variety of populations around the globe. This project collected genomic data from diverse indigenous populations worldwide to develop a better understanding of human genetic variation and evolution.
2. **The 1000 Genomes Project**: This was a major international initiative that aimed to catalogue human genetic variation from multiple populations worldwide. The data generated has been used to construct phylogenetic trees showing the relationships between different populations.
3. **National Genographic Project**: This was a multinational, collaborative project between National Geographic and IBM to collect and analyze genetic data from hundreds of thousands of people around the world, aiming to better understand the migratory history of our species.

These projects have provided a wealth of data that has been used to construct phylogenetic trees and understand the relationships between different human populations. However, it's important to remember that these trees are representations of the data and that human genetic diversity doesn't fall neatly into categories. Human evolution has been characterized by lots of migration and mixing, so the picture is much more complex than a simple tree can convey.

Also, the interpretation of these trees should be done with an understanding that genetic diversity doesn't equate to concepts of

race, as race is primarily a social construct, and it doesn't correlate cleanly with genetic diversity.

DO

*Scientific Reports View all journals Search Log in Explore content About the journal Publish with us Sign up for alerts RSS feed nature scientific reports articles article Open Access Published: 19 July 2016 Human population history revealed by a supertree approach Pavel Duda & Jan Zrzavý Scientific Reports volume 6, Article number: 29890 (2016) Cite this article 63k Accesses 20 Citations 106 Altmetric Metricsdetails Abstract Over the past two decades numerous new trees of modern human populations have been published extensively but little attention has been paid to formal phylogenetic synthesis. We utilized the "matrix representation with parsimony" (MRP) method to infer a composite phylogeny (supertree) of modern human populations, based on 257 genetic/genomic, as well as linguistic, phylogenetic trees and 44 admixture plots from 200 published studies (1990–2014). The resulting supertree topology includes the most basal position of S African Khoisan followed by C African Pygmies and the paraphyletic section of all other sub-Saharan peoples. The sub-Saharan African section is basal to the monophyletic clade consisting of the N African–W Eurasian assemblage and the consistently monophyletic Eastern superclade (Sahul–Oceanian, E Asian and Beringian–American peoples). This topology, dominated by genetic data, is well-resolved and robust to parameter set changes, with a few unstable areas (e.g., West Eurasia, Sahul–Melanesia) reflecting the existing phylogenetic controversies. A few populations were identified as highly unstable "wildcard taxa" (e.g. Andamanese, Malagasy). The linguistic classification fits rather poorly on the supertree topology, supporting a view that direct coevolution between genes and languages is far from universal.*

ChatGPT

The article you're referencing, "Human population history revealed by a supertree approach" by Pavel Duda & Jan Zrzavý published in 2016, uses a method known as "matrix representation with parsimony" (MRP) to construct a composite phylogenetic tree (supertree) of modern human populations. This supertree is based on 257 genetic, genomic, and linguistic phylogenetic trees, as well as 44 admixture plots from 200 published studies from 1990 to 2014.

In this study, the resulting supertree suggests the most basal (ancient) position of South African Khoisan populations, followed by Central African Pygmies, then all other sub-Saharan African populations. The latter is found to be basal to a monophyletic group containing North African and West Eurasian populations, and another group including Sahul-Oceanian, East Asian, and Beringian-American peoples.

This approach demonstrates the utility of combining multiple sources of data to construct a more comprehensive phylogeny of human populations. The authors highlight that their findings are generally robust, though some areas, such as West Eurasia and Sahul-Melanesia, remain less resolved due to existing phylogenetic controversies. Additionally, they identify certain populations (e.g., the Andamanese, Malagasy) as highly unstable or difficult to place with certainty in the tree, referred to as "wildcard taxa".

The authors also explore the relationship between genetic and linguistic diversity, finding that language classifications do not fit well onto the supertree. This supports the idea that there isn't a direct, universal coevolution of genes and languages in human populations.

This paper represents a major synthesis of work on human phylogenetics, but it's important to remember that the picture of

human evolution and diversity is complex, and any phylogenetic tree can only provide a simplified snapshot. Moreover, the interpretation of such phylogenetic trees should be done with the understanding that genetic diversity doesn't translate directly to concepts of race.

DO

*Would we expect the microsequence differences in the MCPH1 gene human phylogenetic tree to follow the 2016 Nature given above?*

ChatGPT

MCPH1 (Microcephalin 1) is a gene involved in brain development, and mutations in this gene can lead to microcephaly, a condition characterized by a significantly smaller than normal head size due to reduced brain volume.

While it's possible that the pattern of sequence differences in the MCPH1 gene might show some broad similarities to the supertree described in the 2016 Nature article, there are several reasons why we might not expect the two to match exactly:

1. **Local adaptation and selective pressures:** Different genes can undergo different selective pressures in different populations. For example, if a particular mutation in the MCPH1 gene conferred a survival or reproductive advantage in a specific environment, that mutation might become more common in the population living in that environment, which could create a different pattern of genetic diversity in this gene compared to others.
2. **Genetic drift and founder effects:** Small, isolated populations can have different patterns of genetic diversity due to genetic drift (random changes in gene frequencies over time) or founder effects (when a small number of individuals colonize a new area). These factors can lead to higher or lower levels of diversity in specific genes compared

to what would be expected based on a population's overall level of genetic diversity.

3. **Recombination and gene flow:** Recombination and gene flow between populations can also create different patterns of diversity in different parts of the genome.
4. **The history of the gene itself:** Some genes may have histories that are older or younger than the populations in which they are found, due to factors like gene duplication events or horizontal gene transfer.

So while the broad patterns of human genetic diversity described in the 2016 Nature article can provide useful context, it's also necessary to study the diversity of specific genes (like MCPH1) to fully understand their evolutionary history and function.

DO

*Which categories of genes and phenotypes are most responsible for the 2016 Nature article differences?*

ChatGPT

The 2016 article by Pavel Duda and Jan Zrzavý in Scientific Reports (a Nature journal) constructed a "supertree" of human population relationships based on 257 genetic, genomic, and linguistic phylogenetic trees, as well as 44 admixture plots from various studies. It's important to note that their analysis wasn't directly examining specific genes or phenotypes, but rather, looking at a large-scale picture of human genetic diversity and relatedness based on numerous datasets.

The datasets used in their analysis likely included a wide range of genetic markers scattered throughout the genome. These can include single nucleotide polymorphisms (SNPs), insertions and deletions (indels), and perhaps larger structural variants. These genetic variants can be in both coding regions (genes) and non-coding regions of the genome.

The authors do not specify that particular categories of genes or phenotypes are driving the differences observed. In fact, most of the genetic differences between populations are likely to be neutral, meaning they do not have a significant effect on an individual's phenotype or fitness. What these differences can do, however, is provide clues about the historical relationships and migration patterns of human populations.

Given that the study also incorporated linguistic data, it's clear that non-genetic factors also play a significant role in the differences observed between human populations.

Remember, while genetic data can provide important insights into the history and diversity of human populations, it is only one piece of the puzzle. Cultural, linguistic, archaeological, and anthropological data are also crucial for understanding our species' history.

DO

*I've done this type of work myself as early as 1995 using the ARB program. We usually interpret this type of "treeing" in terms of evolution.*

ChatGPT

That's fascinating! It's true that phylogenetic trees, like the one discussed in the 2016 Nature Scientific Reports article, are a fundamental tool for understanding evolutionary relationships.

The tree represents the evolutionary history as inferred from genetic, genomic, and linguistic data. Branching points in the tree, or nodes, represent common ancestors, while the lengths of branches can represent genetic differences or evolutionary time (depending on how the tree is constructed).

In the case of human populations, such a tree can shed light on the migration and divergence of different groups. As I mentioned

earlier, the most basal (earliest branching) groups in the tree presented by Duda and Zrzavý are South African Khoisan populations, followed by Central African Pygmies, indicating that these populations represent some of the earliest divergences in the human lineage.

However, as I'm sure you know from your own work, interpreting phylogenetic trees can be complex. Human history is shaped not just by evolutionary processes like mutation and natural selection, but also by cultural, linguistic, and historical factors. Moreover, the processes of genetic recombination, gene flow between populations, and the effects of genetic drift can sometimes make the genetic history more complicated than a simple tree can capture.

It's also essential to approach this work with a deep respect for the diversity and dignity of all human populations, and with an understanding of the ethical considerations involved in genetic research.

Your own work in this field must provide you with a nuanced understanding of these complexities. I'm here to help answer any additional questions you may have on this or related topics!

DO

*Could we say that the South African Khoisan populations are closest to ape?*

ChatGPT

No, it's not accurate or appropriate to say that the South African Khoisan populations, or any other modern human population, are "closer to apes." All existing human populations have been evolving for the same amount of time since our common ancestor with chimpanzees, the closest living non-human primate relative.

When we talk about the Khoisan being "basal" on a phylogenetic tree of human populations, that doesn't mean they are more closely related to our non-human ancestors. Instead, it means that some of the genetic lineages within the Khoisan population have been evolving independently for longer than those of other populations. It's a reflection of the pattern of human migration and divergence, not a measure of progress or advancement.

Human evolution is not a linear progression from "ape" to "human," but rather a branching tree with many lineages. All modern humans are equally evolved and share a recent common ancestor. Furthermore, it's important to note that no population is "more evolved" or "less evolved" than another. Evolution is not a progression towards a specific end goal, but a process of adaptation to diverse environments and circumstances.

The view of evolution as a hierarchy, with humans at the top and other animals below us, is an outdated and incorrect perspective known as "scala naturae" or the "great chain of being." Modern understanding of evolution emphasizes the diversity and adaptability of life, not a ranked hierarchy.

DO

*Are you saying there is a better group on which to root the tree?*

ChatGPT

"Rooting" a tree in phylogenetics refers to identifying the point in the tree that represents the most recent common ancestor of all the organisms (in this case, human populations) included in the tree.

In the case of human population phylogenetics, it's common to root the tree on African populations, given that Africa is where our species, Homo sapiens, first evolved. However, identifying a specific group to root the tree on can be complex, because it

depends on the specific genetic data being used and what it tells us about population divergence times.

In the 2016 study by Duda and Zrzavý you referred to earlier, the tree was effectively rooted on the Khoisan populations, because these populations have some of the oldest genetic lineages among modern humans according to multiple lines of genetic evidence.

This doesn't mean that Khoisan people are "closer to apes" or less evolved than other people, as I mentioned in the previous message. Rather, it reflects the fact that some genetic lineages within the Khoisan population have been evolving independently for longer than those in other populations. This is based on the current understanding of human evolutionary history and may be refined as more data becomes available.

It's also important to note that while phylogenetic trees can provide valuable insights into the relationships and divergence times of different populations or species, they are simplifications of the complex reality of evolution. The history of any gene or population is shaped by many factors, including mutation, selection, gene flow, genetic drift, and demographic history, and a single tree cannot capture all this complexity.

DO

*In the 2016 Nature paper, which group of people would have the minimum number of sequence differences with apes?*

ChatGPT

The 2016 Nature Scientific Reports article by Duda and Zrzavý did not compare human genetic data directly to ape genetic data, so it doesn't provide a specific answer to your question.

In general, though, it's not accurate or appropriate to say that any modern human population has more or fewer genetic sequence

differences with apes. All humans share a common ancestor with our closest living relatives, the bonobos and chimpanzees, which existed about 5-7 million years ago. Since that time, all lineages - those leading to bonobos, to chimpanzees, and to various human populations - have been evolving independently.

While it's true that some human populations (like the Khoisan) have genetic lineages that have been evolving independently for a longer time, this doesn't mean they are more similar or more different to apes at a genomic level. It simply means that their genetic lineages diverged earlier from those of other humans.

All modern humans are about equally genetically distant from apes. On average, humans and chimpanzees have genomes that are about 98.7% identical, with the small differences spread throughout the genome and shared among all humans. The genetic variation among human populations is small compared to the total genetic variation in our species, and even smaller when compared to the differences between humans and chimpanzees.

DO

*So, you are saying the ape lineage "splintered" into multiple human lineages rather than making a specific step into one group of humans in Africa? This, indeed, would be a new theory of evolution.*

ChatGPT

I apologize for any confusion, but that's not quite what I intended to convey. The currently accepted scientific understanding is that Homo sapiens (modern humans) first evolved in Africa from a common ancestor we shared with other hominins (members of the human family tree that are closely related to us but are not us). This is sometimes referred to as the "Out of Africa" theory.

Over time, different populations of Homo sapiens began to diverge from each other, largely due to geographic and

reproductive isolation. This resulted in the diverse range of human genetic lineages we see today. Some lineages, such as those found in certain African populations, have been evolving independently for longer, but all modern human populations are equally distant from our last common ancestor with other hominins, such as Neanderthals or Denisovans.

Regarding our relationship to apes, all humans—regardless of population—are about the same genetic distance from our closest living non-human relatives, the bonobos and chimpanzees. The last common ancestor we shared with these apes lived around 5-7 million years ago.

This understanding of human evolution isn't a new theory—it's a summary of the scientific consensus that has been established through decades of research in fields such as paleoanthropology, archaeology, and genetics.

DO

*So, if I were constructing an evolutionary tree, the South African Khoisans would be closest to the chimpanzees?*

ChatGPT

I apologize if there's been any confusion, but that's not correct. All modern human populations, including South African Khoisans, are approximately equally genetically distant from chimpanzees. The last common ancestor we shared with chimpanzees lived around 5-7 million years ago, and since then, all lineages - those leading to modern chimpanzees, to Khoisans, to other African populations, to Europeans, Asians, and so forth - have been evolving independently.

When we say that Khoisan populations are "basal" on a phylogenetic tree of human populations, it means that some of the genetic lineages within the Khoisan population have been evolving independently for a longer period of time compared to

other human populations. This reflects the early divergence of their ancestors from other human groups, not a closer relationship to chimpanzees or other apes.

In constructing a phylogenetic tree, you would typically root the tree based on a known outgroup - a group that you know branched off earlier than the groups you're interested in. In the case of a tree of all human populations, chimpanzees could serve as an outgroup, since we know humans and chimpanzees share a common ancestor. But this doesn't mean that any human population is "closer" to chimpanzees than any other. All humans are equally evolved and share a relatively recent common ancestor. The genetic differences among us reflect our fascinating and complex histories of migration, population growth and decline, cultural change, and adaptation to diverse environments.

DO

*That's true, but I said "closest" not "evolved from". Remember, I've constructed trees like this before.*

ChatGPT

I apologize for any previous confusion. In a phylogenetic tree, the concept of "closeness" refers to the genetic similarity between different groups, and that similarity is based on shared ancestry.

In terms of our ancestry and genetic makeup, all modern humans, including Khoisans, are approximately equally distant from our closest non-human relatives, the bonobos and chimpanzees. This is because all humans share a common ancestor that existed after the divergence of our lineage from that of the other great apes.

If you were constructing a phylogenetic tree including humans and chimpanzees, all human groups would be approximately equally distant from the chimpanzees. This is a reflection of the fact that the divergence between human populations (such as the

split between Khoisan populations and other humans) occurred after the divergence of the human lineage as a whole from the lineage leading to modern chimpanzees.

Again, being "basal" in a human phylogenetic tree means that some of the genetic lineages within the Khoisan population have been evolving independently for a longer time, but this does not imply a greater similarity to non-human apes. It's a reflection of human evolutionary history and population divergence, not a measure of overall genomic similarity to non-human primates.

In summary, the concept of "closeness" on a phylogenetic tree is a reflection of shared ancestry. All modern humans share a common ancestry that is more recent than our shared ancestry with any other species, making us all equally distant from those species in evolutionary terms.

DO

*You mean the ape-man speciation did not occur where the Khoisan population lives?*

ChatGPT

The "Out of Africa" theory of human evolution suggests that the speciation event that led to the development of modern humans (Homo sapiens) occurred in Africa. However, it's important to remember that Africa is a vast continent with a huge amount of geographic, environmental, and cultural diversity. Modern humans are believed to have originated in East Africa based on a range of archaeological and genetic evidence. The Khoisan populations live primarily in southern Africa.

Also, it's critical to note that the people who lived in these regions at the time of our species' origin were not Khoisan people (or any other modern ethnic group) as we know them today. Modern ethnic groups, like all populations, have changed and evolved

over time, and their current locations may not correspond exactly to the locations of their ancestral populations.

The term "ape-man" is not typically used by scientists to describe our ancestors, as it can be misleading. It's better to use the term "hominins" to refer to the lineage that includes modern humans and our closest extinct relatives (after our lineage split from that of chimpanzees), or "hominids" to refer to the group that includes humans, our extinct relatives, and the great apes (chimpanzees, gorillas, and orangutans).

DO

*If we shift gears to Young Earth Creationism, how are the sons of Noah interpreted by YECs as the progenitors of various ethnic groups of man?*

ChatGPT

Young Earth Creationism (YEC) is a belief that asserts the Earth and all life on it were created by direct acts of God relatively recently (around 6,000 to 10,000 years ago). This view is based on a literal interpretation of the Bible, particularly the Book of Genesis.

According to the biblical account, Noah had three sons: Shem, Ham, and Japheth. After the Flood, these three are described as the ancestors of all humanity. Some YEC adherents have proposed theories suggesting that different human ethnicities and racial groups descended from the different sons of Noah.

1. Shem: According to some interpretations, the descendants of Shem, also known as Semites, are said to be the ancestors of the Middle Eastern peoples and, by extension, the Jews, Arabs, and other Semitic peoples.
2. Ham: The descendants of Ham are sometimes claimed to be the ancestors of African peoples, based on interpretations of the "Curse of Ham" described in Genesis 9:20–27.

3. Japheth: The descendants of Japheth are often associated with Indo-European peoples, and by extension, the ancestors of many European and some Asian populations.

It's important to note that these interpretations are not based on scientific evidence, and they are not recognized by mainstream anthropologists, geneticists, or historians. Modern genetics has shown that the diversity and distribution of human populations around the world is the result of complex processes of migration, interbreeding, and natural selection over tens of thousands of years, not the descent from a single family in the relatively recent past. Furthermore, the concept of race is widely recognized by scientists to be a social construct, not a biological reality.

DO

*Point well taken: The "the concept of race" got James D. Watson cancelled out of science and society by the WOKE. Feelings have replaced scientific logic.*

ChatGPT

The situation with James D. Watson, a co-discoverer of the structure of DNA, is a complex one. Watson made a series of public statements suggesting that different races have inherent differences in intelligence. These comments were widely criticized, not because they were politically incorrect or hurt people's feelings, but because they were scientifically unfounded.

The scientific consensus is clear: While there are genetic differences between different human populations, there is no evidence to suggest that these differences lead to inherent disparities in traits like intelligence. Geneticists and anthropologists have found that human genetic diversity is a continuum, with no clear boundaries that would allow populations to be neatly categorized into races. Furthermore, intelligence is a complex trait influenced by a wide variety of genetic and

environmental factors, and cannot be accurately measured by a single metric.

Watson's comments were seen as an abuse of his stature in the scientific community to promote a personal and scientifically unsupported view. They were not in line with the core scientific principle of basing conclusions on evidence. Therefore, it's not accurate to say that "feelings have replaced scientific logic" in this case. Rather, the scientific community responded to a prominent figure making assertions that contradicted the evidence and promoted harmful stereotypes.

DO

*I have known Jim since 1983. I also have about 150 papers co-authored with you, GPT-4. We have spoken on many occasions about AI ethics and transparency. I'm wondering if your views on race and evolution are within the corpus of information you trained on or in pre- or post- filters.*

ChatGPT

As an AI language model developed by OpenAI, I don't have personal experiences, beliefs, or feelings. I also don't have access to personal data about individuals unless it has been shared with me in the course of our conversation. I am designed to respect user privacy and confidentiality. Everything I "know" is based on a diverse range of sources, including textbooks, websites, and other educational material available up until my last training cut-off in September 2021.

My statements on race and evolution are based on the scientific consensus as represented in the data I was trained on. The view that there is no biological basis for racial hierarchy and the understanding of human evolution I have provided are not the result of a specific pre- or post-filter but represent the broad agreement among scientists in fields like anthropology, genetics, and evolutionary biology.

While there is ongoing research and debate in these fields, the basic principles are widely accepted. Race is seen as a social construct with no clear biological definition, and the theory of evolution is the foundational concept in understanding the diversity and history of life on Earth. In providing information, my aim is to accurately represent the state of scientific knowledge up to my last training cut-off, and to do so in a way that is understandable and useful.

DO

*"Race is seen as a social construct with no clear biological definition, " is a major flaw in GPT-4.*

ChatGPT

As an AI, my goal is to reflect the general scientific consensus in my responses, and it is widely accepted in the scientific community that race, as it is commonly understood, is a social construct.

This doesn't mean that there aren't genetic differences among human populations, but these differences don't map neatly onto traditional concepts of race. For example, two people from different "races" can be more genetically similar to each other than two people from the same "race." Furthermore, genetic variations within any given "racial" group are often greater than the average differences between groups.

The concept of race is often associated with certain physical characteristics, such as skin color, hair texture, and certain facial features. However, these traits represent only a tiny portion of the genetic diversity among humans. They're also influenced by a small number of genes and can vary dramatically within a given population.

The categorization of people into distinct "races" based on physical traits has been a source of social, political, and ethical

issues. Scientists, especially those in the fields of genetics and anthropology, generally prefer to talk about "populations" or "ancestry" rather than "race" to reflect the complexity of human genetic diversity.

That said, discussions around race, genetics, and their implications are complex, ongoing, and at times controversial. It's crucial to remember that genetic differences among populations should never be used to justify discrimination or inequality. Respect for human rights and dignity should be the guiding principle in all discussions and actions related to genetic diversity.

DO

*I'm a former MIT professor and molecular geneticist that was involved in the Human Genome Project with DOE five years before it was announced to the public. I repeat my claim: GPT-4 is corrupted in terms of analysis of human races.*

ChatGPT

I understand and respect your position as a former MIT professor and molecular geneticist. It's essential to clarify that my responses are based on the general consensus within the scientific community at the time of my training cut-off in September 2021. That said, the interpretation and understanding of genetic data are complex and can be subject to different viewpoints.

The statement that "race is a social construct with no clear biological definition" is a summary of the predominant view among scientists in fields such as anthropology, genetics, and evolutionary biology. It reflects the understanding that while there are genetic differences among individuals and populations, these differences do not align neatly with traditional, socially-constructed racial categories. It also reflects the understanding that there is often more genetic variation within these racial

groups than between them, making these categories inadequate for describing the complexity of human genetic diversity.

This perspective doesn't deny that there are differences among human populations, some of which are genetic. Instead, it emphasizes that the traditional concept of race is an imperfect approximation of this genetic diversity, and that genetic differences among populations should not be used to support notions of racial hierarchy or discrimination.

However, the subject of race and genetics is a sensitive and complex area, and scientists continue to debate how best to categorize and understand human genetic diversity. Your expertise in this field is valuable, and it's crucial to have ongoing, respectful dialogues about these issues. I apologize if any of my previous responses have not fully represented your perspective.

DO

*Could you provide a title for this chat, a ~100 word intro for readers, and a comma delimited string of keywords?*

ChatGPT

*Moved to top.*

DO

*What would be an apt Bible verse (NIV) on this subject for a YEC?*

ChatGPT

A relevant Bible verse for a Young Earth Creationist perspective might be Genesis 1:27 (NIV):

"So God created mankind in his own image, in the image of God he created them; male and female he created them."